

09/673300  
529 Rec'd CT/PTC 16 OCT 2000

SEQUENCE LISTING

~~Y LIMITED~~  
<110> ~~SUN~~ coding for a protein having glycosyl transferase  
<120> aurone  
<1> 1751  
<12> DNA  
<213> *Antirrhinum majus*  
<220>  
<223> Nucleotide sequence coding for a protein having  
glycosyl transferase to aurone

<400> 1  
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attttccttt taaaa atg gga aaa ctt cac att gcc tta ttt cca gtt atg 111  
Met Gly Lys Leu His Ile Ala Leu Phe Pro Val Met  
1 5 10  
gct cat ggt cac atg atc cca atg ttg gac atg gcc aag ctc ttt acc 159  
Ala His Gly His Met Ile Pro Met Leu Asp Met Ala Lys Leu Phe Thr  
15 20 25  
tca aga ggc ata caa aca aca atc att tcg act ctc gcc ttc gct gat 207  
Ser Arg Gly Ile Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp  
30 35 40  
ccg ata aac aaa gct cgt gat tcg ggc ctc gat att gga cta agc atc 255  
Pro Ile Asn Lys Ala Arg Asp Ser Gly Leu Asp Ile Gly Leu Ser Ile  
45 50 55 60  
ctc aaa ttc cca cca gaa gga tca gga ata cca gat cac atg gtg agc 303  
Leu Lys Phe Pro Pro Glu Gly Ser Gly Ile Pro Asp His Met Val Ser  
65 70 75

1/18

ctt gat cta gtt act gaa gat tgg ctc cca aag ttt gtt gag tca tta 351  
 Leu Asp Leu Val Thr Glu Asp Trp Leu Pro Lys Phe Val Glu Ser Leu  
       80                     85                     90  
 gtc tta tta caa gag cca gtt gag aag ctt atc gaa gaa cta aag ctc 399  
 Val Leu Leu Gln Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu  
       95                     100                     105  
 gac tgt ctc gtt tcc gac atg ttc ttg cct tgg aca gtc gat tgt gcg 447  
 Asp Cys Leu Val Ser Asp Met Phe Leu Pro Trp Thr Val Asp Cys Ala  
       110                     115                     120  
 gct aag ttc ggt att ccg agg ttg gtt ttc cac gga acg acg aac ttt 495  
 Ala Lys Phe Gly Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe  
       125                     130                     135                     140  
 gcg ttg tgt gct tcg gag caa atg aag ctt cac aag cct tat aag aat 543  
 Ala Leu Cys Ala Ser Glu Gln Met Lys Leu His Lys Pro Tyr Lys Asn  
       145                     150                     155  
 gta act tct gat act gag aca ttt gtt ata ccg gat ttc ccg cat gag 591  
 Val Thr Ser Asp Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu  
       160                     165                     170  
 ctg aag ttt gtg agg act caa gtg gct ccg ttt cag ctt gcg gaa acg 639  
 Leu Lys Phe Val Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr  
       175                     180                     185  
 gag aat gga ttc tca aag ttg atg aaa cag atg acg gag tct gtt ggt 687  
 Glu Asn Gly Phe Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly  
       190                     195                     200  
 aga agc tac ggt gtt gtg gtt aac agt ttt tat gag ctc gag tcg act 735  
 Arg Ser Tyr Gly Val Val Val Asn Ser Phe Tyr Glu Leu Glu Ser Thr  
       205                     210                     215                     220  
 tat gtg gat tat tac aga gag gtt ttg ggt aga aag tat tgg aat ata 783  
 Tyr Val Asp Tyr Tyr Arg Glu Val Leu Gly Arg Lys Ser Trp Asn Ile  
       225                     230                     235  
 ggg cct ctg ttg tta tcc aac aat ggc aat gag gaa aaa gta caa agg 831  
 Gly Pro Leu Leu Leu Ser Asn Asn Gly Asn Glu Glu Lys Val Gln Arg  
       240                     245                     250  
 gga aag gaa tct gcg att ggc gaa cac gaa tgc ttg gct tgg ttg aat 879  
 Gly Lys Glu Ser Ala Ile Gly Glu His Glu Cys Leu Ala Trp Leu Asn  
       255                     260                     265

tcc aag aag cag aat tcg gtt gtt tac gtt ttt gga agt atg gcg	927
Ser Lys Lys Gln Asn Ser Val Val Tyr Val Cys Phe Gly Ser Met Ala	
270 275 280	
act ttt act cca gcg cag ttg cgc gaa act gcg att gga ctc gag gaa	975
Thr Phe Thr Pro Ala Gln Leu Arg Glu Thr Ala Ile Gly Leu Glu Glu	
285 290 295 300	
tca ggc caa gag ttc att tgg gta gtt aaa aag gcc aaa aac gaa gaa	1023
Ser Gly Gln Glu Phe Ile Trp Val Val Lys Lys Ala Lys Asn Glu Glu	
305 310 315	
gaa gga aaa gga aaa gaa gaa tgg ctg cca gaa aat ttt gag gaa aga	1071
Glu Gly Lys Gly Glu Trp Leu Pro Glu Asn Phe Glu Glu Arg	
320 325 330	
gtg aaa gat aga ggc ttg atc ata aga gga tgg gcg cca ttg ttg	1119
Val Lys Asp Arg Gly Leu Ile Ile Arg Gly Trp Ala Pro Gln Leu Leu	
335 340 345	
ata ctc gat cat cct gcg gta gga gct ttc gtg acg cat tgt gga tgg	1167
Ile Leu Asp His Pro Ala Val Gly Ala Phe Val Thr His Cys Gly Trp	
350 355 360	
aat tcg acg ttg gaa gga ata tgc gcc ggt gtg cct atg gtg act tgg	1215
Asn Ser Thr Leu Glu Gly Ile Cys Ala Gly Val Pro Met Val Thr Trp	
365 370 375 380	
cca gtt ttc gca gag cag ttt ttc aat gag aag ttt gtg aca gag gtt	1263
Pro Val Phe Ala Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Glu Val	
385 390 395	
ttg ggg acc ggt gtt tcg gtt ggg aat aag aag tgg cta agg gca gca	1311
Leu Gly Thr Gly Val Ser Val Gly Asn Lys Lys Trp Leu Arg Ala Ala	
400 405 410	
agt gaa ggt gtg tcg agg gag gca gtg acg aac gca gtg cag cgt gtt	1359
Ser Glu Gly Val Ser Arg Glu Ala Val Thr Asn Ala Val Gln Arg Val	
415 420 425	
atg gtg gga gaa aat gcg tcg gag atg aga aag cga ggg aag tat tat	1407
Met Val Gly Glu Asn Ala Ser Glu Met Arg Lys Arg Ala Lys Tyr Tyr	
430 435 440	
aag gaa atg gcg agg cgg gcg gtt gag gaa ggc ggt tcg tct tat aat	1455
Lys Glu Met Ala Arg Arg Ala Val Glu Glu Gly Gly Ser Ser Tyr Asn	
445 450 455 460	

ggt ttg aat gag atg ata gag gat ttg agt gtg tac cgt gct cca gaa 1503  
Gly Leu Asn Glu Met Ile Glu Asp Leu Ser Val Tyr Arg Ala Pro Glu  
465 470 475  
aaa caa gac tta aac tagattctta tagatgactt ctagtgtgac aattgtaatt 1558  
Lys Gln Asp Leu Asn  
480  
ttttgcctt tattcaagtt tcctcattag tggtagagc ttccctgta tttcagaat 1618  
tggttgttc aattttaca tgatttgta tagatagctg catagttct agctgttaac 1678  
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aaaaaaaaaaa aaa 1751

<210> 2

<211> 481

<212> PRT

<213> *Antirrhinum majus*

<220>

<223> Amino acid sequence of a protein having glycosyl transferase to aurone

<400> 2

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Met Ile Pro Met Leu Asp Met Ala Lys Leu Phe Thr Ser Arg Gly Ile  
20 25 30  
Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp Pro Ile Asn Lys  
35 40 45  
Ala Arg Asp Ser Gly Leu Asp Ile Gly Leu Ser Ile Leu Lys Phe Pro  
50 55 60  
Pro Glu Gly Ser Gly Ile Pro Asp His Met Val Ser Leu Asp Leu Val  
65 70 75 80  
Thr Glu Asp Trp Leu Pro Lys Phe Val Glu Ser Leu Val Leu Lys Gln  
85 90 95  
Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu Asp Cys Leu Val  
100 105 110  
Ser Asp Met Phe Leu Pro Trp Thr Val Asp Cys Ala Ala Lys Phe Gly  
115 120 125

Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe Ala Leu Cys Ala  
130 135 140  
Ser Glu Gln Met Lys Leu His Lys Pro Tyr Lys Asn Val Thr Ser Asp  
145 150 155 160  
Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu Leu Lys Phe Val  
165 170 175  
Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr Glu Asn Gly Phe  
180 185 190  
Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly Arg Ser Tyr Gly  
195 200 205  
Val Val Val Asn Ser Phe Tyr Glu Leu Glu Ser Thr Tyr Val Asp Tyr  
210 215 220  
Tyr Arg Glu Val Leu Gly Arg Lys Ser Trp Asn Ile Gly Pro Leu Leu  
225 230 235 240  
Leu Ser Asn Asn Gly Asn Glu Glu Lys Val Gln Arg Gly Lys Glu Ser  
245 250 255  
Ala Ile Gly Glu His Glu Cys Leu Ala Trp Leu Asn Ser Lys Lys Gln  
260 265 270  
Asn Ser Val Val Tyr Val Cys Phe Gly Ser Met Ala Thr Phe Thr Pro  
275 280 285  
Ala Gln Leu Arg Glu Thr Ala Ile Gly Leu Glu Glu Ser Gly Gln Glu  
290 295 300  
Phe Ile Trp Val Val Lys Lys Ala Lys Asn Glu Glu Glu Gly Lys Gly  
305 310 315 320  
Lys Glu Glu Trp Leu Pro Glu Asn Phe Glu Glu Arg Val Lys Asp Arg  
325 330 335  
Gly Leu Ile Ile Arg Gly Trp Ala Pro Gln Leu Leu Ile Leu Asp His  
340 345 350  
Pro Ala Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu  
355 360 365  
Glu Gly Ile Cys Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala  
370 375 380  
Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Glu Val Leu Gly Thr Gly  
385 390 395 400  
Val Ser Val Gly Asn Lys Lys Trp Leu Arg Ala Ala Ser Glu Gly Val  
405 410 415  
Ser Arg Glu Ala Val Thr Asn Ala Val Gln Arg Val Met Val Gly Glu  
420 425 430

Asn Ala Ser Glu Met Arg Lys Arg Ala Lys Tyr Tyr Lys Glu Met Ala  
435 440 445  
Arg Arg Ala Val Glu Glu Gly Ser Ser Tyr Asn Gly Leu Asn Glu  
450 455 460  
Met Ile Glu Asp Leu Ser Val Tyr Arg Ala Pro Glu Lys Gln Asp Leu  
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Asn

<210> 3

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400>

ataaactacat atgggacaaac tccac

25

<210> 4

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 4

cagaacagga tccacacgta attta

25

<210> 5

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 5  
ataactacat atggaaaaac ttcac

25

<210> 6  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 6  
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26

<210> 7  
<211> 1750  
<212> DNA  
<213> Petunia hybrida

<220>  
<223> Nucleotide sequence coding for a protein having  
glycosyl transferase to aurone

<400> 7  
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Met Ala Ile Pro Thr Val

53

10  
caa cca cat ttt gtg ctg ctt cct ttc atg gca caa ggc cat aca aat  
Gln Pro His Phe Val Leu Leu Pro Phe Met Ala Gln Gly His Thr Asn

101

15  
ccc atg att gac atc gca cgc cta ttg gca caa cgc gga gtt ata atc  
Pro Met Ile Asp Ile Ala Arg Leu Leu Ala Gln Arg Gly Val Ile Ile

149

20  
acc att ctt act aca cac ttt aat gcc act aga ttc aag aca gtc gtt  
Thr Ile Leu Thr Thr His Phe Asn Ala Thr Arg Phe Lys Thr Val Val

197

40

45

50

gat cgg gca gta gtg gca gca cta aag att cag gta gtt cac ctc tat 245  
 Asp Arg Ala Val Val Ala Ala Leu Lys Ile Gln Val Val His Leu Tyr  
 55 60 65 70  
 ttt cca agc tta gag gct gga cta cct gaa ggg tgt gaa gct ttc gac 293  
 Phe Pro Ser Leu Glu Ala Gly Leu Pro Glu Gly Cys Glu Ala Phe Asp  
 75 80 85  
 atg ctt cct tca atg gat ttc gca atg aaa ttc ttt gat gct acc agt 341  
 Met Leu Pro Ser Met Asp Phe Ala Met Lys Phe Phe Asp Ala Thr Ser  
 90 95 100  
 agg ctt caa cca caa gtg gaa gaa atg ctt cat gaa ctg caa ccg tca 389  
 Arg Leu Gln Pro Gln Val Glu Glu Met Leu His Glu Leu Gln Pro Ser  
 105 110 115  
 cca agt tgc ata ata tct gat atg tgt ttt cca tgg aca act aat gtt 437  
 Pro Ser Cys Ile Ile Ser Asp Met Cys Phe Pro Trp Thr Thr Asn Val  
 120 125 130  
 gca caa aaa ttc aac att cct agg ctt gtt ttt cat ggg atg tgc tgt 485  
 Ala Gln Lys Phe Asn Ile Pro Arg Leu Val Phe His Gly Met Cys Cys  
 135 140 145 150  
 ttt tct tta ttg tgc ttg cac aat ttg aga gat tgg aag gag ttg gag 533  
 Phe Ser Leu Leu Cys Leu His Asn Leu Arg Asp Trp Lys Glu Leu Glu  
 155 160 165  
 tct gat ata gaa tat ttt caa gtt cca gga tta cat gac aaa att gaa 581  
 Ser Asp Ile Glu Tyr Phe Gln Val Pro Gly Leu His Asp Lys Ile Glu  
 170 175 180  
 tta aac aaa gct cag ctt tca aat att gtt aag cca aga ggt cct gat 629  
 Leu Asn Lys Ala Gln Leu Ser Asn Ile Val Lys Pro Arg Gly Pro Asp  
 185 190 195  
 tgg aat gaa ttt gca gat caa ctg aag aaa gca gaa gaa gaa gct tat 677  
 Trp Asn Glu Phe Ala Asp Gln Leu Lys Lys Ala Glu Glu Ala Tyr  
 200 205 210  
 ggg ata gta gct aat agc ttt gaa gag tta gaa cca gaa tat gtc aag 725  
 Gly Ile Val Ala Asn Ser Phe Glu Glu Leu Glu Pro Glu Tyr Val Lys  
 215 220 225 230  
 gga ttg gaa aag gca aaa ggc ttg aaa att tgg cca att ggt cct gtt 773  
 Gly Leu Glu Lys Ala Lys Gly Leu Lys Ile Trp Pro Ile Gly Pro Val  
 235 240 245

tct ttg tgc aac aaa gag aaa cag gac aag gct gaa aga gga aac aag 821  
 Ser Leu Cys Asn Lys Glu Lys Gln Asp Lys Ala Glu Arg Gly Asn Lys  
 250 255 260  
 gct tca att gat gaa cac cag tgt cta aaa tgg cta gat tct tgg gga 869  
 Ala Ser Ile Asp Glu His Gln Cys Leu Lys Trp Leu Asp Ser Trp Gly  
 265 270 275  
 gca aac tct gta ctc ttt gta tgt ctc ggg agc cta tcg cgc ctt cca 917  
 Ala Asn Ser Val Leu Phe Val Cys Leu Gly Ser Leu Ser Arg Leu Pro  
 280 285 290  
 acg cca caa atg ata gag ctg gga ctt ggc tta gaa tcg tcg aaa aga 965  
 Thr Pro Gln Met Ile Glu Leu Gly Leu Gly Leu Glu Ser Ser Lys Arg  
 295 300 305 310  
 ccc ttt att tgg gtt gtt aga cac aag tca gat gaa ttt aaa agt tgg 1013  
 Pro Phe Ile Trp Val Val Arg His Lys Ser Asp Glu Phe Lys Ser Trp  
 315 320 325  
 cta gtt gaa gaa aat ttt gag gaa aga gtt aaa gga caa gga ctt tta 1061  
 Leu Val Glu Glu Asn Phe Glu Glu Arg Val Lys Gly Gln Gly Leu Leu  
 330 335 340  
 atc cat ggt tgg gca cca caa gta cta ata tta tct cac act tca att 1109  
 Ile His Gly Trp Ala Pro Gln Val Leu Ile Leu Ser His Thr Ser Ile  
 345 350 355  
 gga gga ttc ttg act cat tgt gga tgg aat tcg agt gtc gaa gga ata 1157  
 Gly Gly Phe Leu Thr His Cys Gly Trp Asn Ser Ser Val Glu Gly Ile  
 360 365 370  
 tct gca ggc gtt cca atg atc act tgg cca atg ttt gct gaa caa ttc 1205  
 Ser Ala Gly Val Pro Met Ile Thr Trp Pro Met Phe Ala Glu Gln Phe  
 375 380 385 390  
 tgt aat gaa agg cta ata gtg aat gta ctg aag aca gga gta aag gct 1253  
 Cys Asn Glu Arg Leu Ile Val Asn Val Leu Lys Thr Gly Val Lys Ala  
 395 400 405  
 gga att gag aat cct gtt atg ttt gga gag gaa gaa aaa gtt gga gca 1301  
 Gly Ile Glu Asn Pro Val Met Phe Gly Glu Glu Lys Val Gly Ala  
 410 415 420  
 caa gtg agc aaa gat gat att aag atg gtt att gaa aga gtc atg ggc 1349  
 Gln Val Ser Lys Asp Asp Ile Lys Met Val Ile Glu Arg Val Met Gly  
 425 430 435

gaa gaa gag gaa gct gaa atg aga aga aaa aga gca aaa gag tta gga 1397  
Glu Glu Glu Glu Ala Glu Met Arg Arg Lys Arg Ala Lys Glu Leu Gly  
440 445 450  
gaa aag gca aag agg gct atg gag gaa ggg ggt tcc tca cac ttc aac 1445  
Glu Lys Ala Lys Arg Ala Met Glu Glu Gly Ser Ser His Phe Asn  
455 460 465 470  
ttg aca cag ttg att caa gat gtc act gag caa gca aat att tta aaa 1493  
Leu Thr Gln Leu Ile Gln Asp Val Thr Glu Gln Ala Asn Ile Leu Lys  
475 480 485  
tcc atc taggattata aagtcgattc caagttcctt ttacgatcaa tttctaacc 1549  
Ser Ile  
tctactagag atggtaacaa tccaaactgc gcctttttg cacaataatt attgtttat 1609  
gttcagctag cacaaaaagt ttactattag tagaaatatt tcagctggaa ctgcccgaact 1669  
gctatgtaca ctgatggAAC aatgtatgtc atgctattca aattaactct gagctgaaaa 1729  
tatcatatag gagctgatTT t 1750

<210> 8

<211> 488

<212> PRT

<213> Petunia hybrida

<220>

<223> Amino acid sequence of a protein having glycosyl transferase to aurone

<400> 8

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Ala Gln Gly His Thr Asn Pro Met Ile Asp Ile Ala Arg Leu Leu Ala  
20 25 30  
Gln Arg Gly Val Ile Ile Thr Ile Leu Thr Thr His Phe Asn Ala Thr  
35 40 45  
Arg Phe Lys Thr Val Val Asp Arg Ala Val Val Ala Ala Leu Lys Ile  
50 55 60  
Gln Val Val His Leu Tyr Phe Pro Ser Leu Glu Ala Gly Leu Pro Glu  
65 70 75 80  
Gly Cys Glu Ala Phe Asp Met Leu Pro Ser Met Asp Phe Ala Met Lys  
85 90 95

Phe Phe Asp Ala Thr Ser Arg Leu Gln Pro Gln Val Glu Glu Met Leu  
100 105 110  
His Glu Leu Gln Pro Ser Pro Ser Cys Ile Ile Ser Asp Met Cys Phe  
115 120 125  
Pro Trp Thr Thr Asn Val Ala Gln Lys Phe Asn Ile Pro Arg Leu Val  
130 135 140  
Phe His Gly Met Cys Cys Phe Ser Leu Leu Cys Leu His Asn Leu Arg  
145 150 155 160  
Asp Trp Lys Glu Leu Glu Ser Asp Ile Glu Tyr Phe Gln Val Pro Gly  
165 170 175  
Leu His Asp Lys Ile Glu Leu Asn Lys Ala Gln Leu Ser Asn Ile Val  
180 185 190  
Lys Pro Arg Gly Pro Asp Trp Asn Glu Phe Ala Asp Gln Leu Lys Lys  
195 200 205  
Ala Glu Glu Glu Ala Tyr Gly Ile Val Ala Asn Ser Phe Glu Glu Leu  
210 215 220  
Glu Pro Glu Tyr Val Lys Gly Leu Glu Lys Ala Lys Gly Leu Lys Ile  
225 230 235 240  
Trp Pro Ile Gly Pro Val Ser Leu Cys Asn Lys Glu Lys Gln Asp Lys  
245 250 255  
Ala Glu Arg Gly Asn Lys Ala Ser Ile Asp Glu His Gln Cys Leu Lys  
260 265 270  
Trp Leu Asp Ser Trp Gly Ala Asn Ser Val Leu Phe Val Cys Leu Gly  
275 280 285  
Ser Leu Ser Arg Leu Pro Thr Pro Gln Met Ile Glu Leu Gly Leu Gly  
290 295 300  
Leu Glu Ser Ser Lys Arg Pro Phe Ile Trp Val Val Arg His Lys Ser  
305 310 315 320  
Asp Glu Phe Lys Ser Trp Leu Val Glu Glu Asn Phe Glu Glu Arg Val  
325 330 335  
Lys Gly Gln Gly Leu Leu Ile His Gly Trp Ala Pro Gln Val Leu Ile  
340 345 350  
Leu Ser His Thr Ser Ile Gly Gly Phe Leu Thr His Cys Gly Trp Asn  
355 360 365  
Ser Ser Val Glu Gly Ile Ser Ala Gly Val Pro Met Ile Thr Trp Pro  
370 375 380  
Met Phe Ala Glu Gln Phe Cys Asn Glu Arg Leu Ile Val Asn Val Leu  
385 390 395 400

Lys Thr Gly Val Lys Ala Gly Ile Glu Asn Pro Val Met Phe Gly Glu  
405 410 415  
Glu Glu Lys Val Gly Ala Gln Val Ser Lys Asp Asp Ile Lys Met Val  
420 425 430  
Ile Glu Arg Val Met Gly Glu Glu Glu Ala Glu Met Arg Arg Lys  
435 440 445  
Arg Ala Lys Glu Leu Gly Glu Lys Ala Lys Arg Ala Met Glu Glu Gly  
450 455 460  
Gly Ser Ser His Phe Asn Leu Thr Gln Leu Ile Gln Asp Val Thr Glu  
465 470 475 480  
Gln Ala Asn Ile Leu Lys Ser Ile  
485

<210> 9

<211> 1669

<212> DNA

<213> Petunia hybrida

<220>

<223> Nucleotide sequence coding for a protein having  
glycosyl transferase to aurone

<400> 9

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tgctaagtac tactactagt acacatctt ctttctatca aacactttcc aaa atg 116  
Met

1

ggt cag ctc cat ttt ttc ttc ttt ccc atg atg gct cat ggc cac atg 164  
Gly Gln Leu His Phe Phe Phe Pro Met Met Ala His Gly His Met  
5 10 15

att cct aca cta gac atg gct aag ctt ttc gct tca cgt ggt gtt aag 212  
Ile Pro Thr Leu Asp Met Ala Lys Leu Phe Ala Ser Arg Gly Val Lys  
20 25 30

gcc acc ata atc act act cct ctc aat gaa tca gtt ttc tcc aaa gct 260  
Ala Thr Ile Ile Thr Pro Leu Asn Glu Ser Val Phe Ser Lys Ala  
35 40 45

att gaa aga aac aag cat gaa att gac atc cgt ttg atc aaa ttc caa 308  
 Ile Glu Arg Asn Lys His Glu Ile Asp Ile Arg Leu Ile Lys Phe Gln  
 50 55 60 65  
 gct gtt gaa aat ggc ttg cct gaa ggt tgt gag cgt att gat ctt atc 356  
 Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu Ile  
 70 75 80  
 cct tct gat gac aag ctt tcc aat ttt ttg aaa gct gca gct atg atg 404  
 Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Ala Met Met  
 85 90 95  
 caa gaa cca ctt gag cag ctt att gaa gaa tgt cat ccc aat tgt ctt 452  
 Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys Leu  
 100 105 110  
 gtt tct gat atg ttc ctt cct tgg act act gat act gca gcc aag ttt 500  
 Val Ser Asp Met Phe Leu Pro Trp Thr Thr Asp Thr Ala Ala Lys Phe  
 115 120 125  
 aac att cca aga ata gtt ttc cat ggt acg agt ttc ttt gca ctt tgt 548  
 Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu Cys  
 130 135 140 145  
 gta gag aat agt aac agg act aat aag cca ttc aag aac gtc tct tct 596  
 Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser Ser  
 150 155 160  
 gat tct gaa act ttt gtt gta cca aat ttg cct cac gaa atc agg cta 644  
 Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg Leu  
 165 170 175  
 act aga aca caa ttg tct ccg ttt gag caa tca ttg gaa gag aca cca 692  
 Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr Pro  
 180 185 190  
 atg tcc cga atg ata aaa gca gtt agg gaa tcg gac gcg aag agt tat 740  
 Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser Tyr  
 195 200 205  
 gga gtt atc ttc aac agc ttc tat gag ctt gaa tca gat tat gtt gaa 788  
 Gly Val Ile Phe Asn Ser Phe Tyr Glu Leu Glu Ser Asp Tyr Val Glu  
 210 215 220 225  
 cat tat acc aag gtt ctt ggt aga aag tct tgg gct att ggc ccg ctt 836  
 His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro Leu  
 230 235 240

ttt ttg tgc aat agg gac att gaa gat aaa gct gaa aga ggg aag att	884
Ser Leu Cys Asn Arg Asp Ile Glu Asp Lys Ala Glu Arg Gly Lys Ile	
245 250 255	
tcc tct att gat aaa cat gag tgt ttg aat tgg ctt gat tca aag aaa	932
Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys Lys	
260 265 270	
cca agt tcc att gtt tat gtt tgc ttc ggg agc gta gca gat ttc act	980
Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe Thr	
275 280 285	
gca gca caa atg cgt gaa ctt gca ttg gga att gaa gca tct gga caa	1028
Ala Ala Gln Met Arg Glu Leu Ala Leu Gly Ile Glu Ala Ser Gly Gln	
290 295 300 305	
gaa ttc att tgg gct gtt aga aga ggc aaa gag gaa caa gac aat gaa	1076
Glu Phe Ile Trp Ala Val Arg Arg Gly Lys Glu Glu Gln Asp Asn Glu	
310 315 320	
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Glu Trp Leu Pro Glu Gly Phe Glu Glu Arg Thr Lys Glu Lys Gly Leu	
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att att aga gga tgg gcg ccc caa gtg cta att ctt gat cac caa gct	1172
Ile Ile Arg Gly Trp Ala Pro Gln Val Leu Ile Leu Asp His Gln Ala	
340 345 350	
gtg gga gct ttt gtc act cat tgt ggt tgg aat tca acg ctt gaa gga	1220
Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu Gly	
355 360 365	
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Val Ser Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala Glu Gln	
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Phe Phe Asn Glu Lys Leu Val Thr Glu Val Leu Arg Thr Gly Ala Gly	
390 395 400	
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Val Gly Ser Met Gln Trp Lys Arg Ser Ala Ser Glu Gly Val Lys Arg	
405 410 415	
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Glu Ala Ile Ala Lys Ala Ile Lys Arg Val Met Val Ser Glu Glu Ala	
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Glu Gly Phe Arg Asn Arg Ala Lys Ala Tyr Lys Glu Met Ala Lys Gln  
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Ala Ile Glu Glu Gly Gly Ser Ser Tyr Ser Gly Leu Thr Thr Leu Leu  
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caa gat ata agt aca tat agt tcc aaa agt cat taactgcaca actaaaaaaaa 1561  
Gln Asp Ile Ser Thr Tyr Ser Ser Lys Ser His  
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tgtagtgttg ttctatacaa ttttatgct ttttatgcg tgtactaatt taaacatgga 1621  
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35 40 45  
Ala Ile Glu Arg Asn Lys His Glu Ile Asp Ile Arg Leu Ile Lys Phe  
50 55 60  
Gln Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu  
65 70 75 80  
Ile Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Met  
85 90 95  
Met Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys  
100 105 110  
Leu Val Ser Asp Met Phe Leu Pro Trp Thr Asp Thr Ala Ala Lys  
115 120 125

Phe Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu  
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Cys Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser  
145 150 155 160  
Ser Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg  
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Leu Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr  
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Pro Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser  
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Glu His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro  
225 230 235 240  
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245 250 255  
Ile Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys  
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Lys Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe  
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Gln Glu Phe Ile Trp Ala Val Arg Arg Gly Lys Glu Glu Gln Asp Asn  
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Glu Glu Trp Leu Pro Glu Gly Phe Glu Glu Arg Thr Lys Glu Lys Gly  
325 330 335  
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355 360 365  
Gly Val Ser Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala Glu  
370 375 380  
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385 390 395 400  
Gly Val Gly Ser Met Gln Trp Lys Arg Ser Ala Ser Glu Gly Val Lys  
405 410 415  
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420 425 430

Ala Glu Gly Phe Arg Asn Arg Ala Lys Ala Tyr Lys Glu Met Ala Lys  
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